

**Figure 10A-10C** The representative prokaryotic phylogenetic tree in Newick format.

**Figure 10A**

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'<Msr.barker> Methanosarcina barkeri str. 227 DSM 1538' : 0.13236 , '<Msp.hungat> Methanospirillum hungatei str. JF1 DSM 864 (T)' : 0.16948 ) : 0.24421 , '<Hf.volcani> Haloferax volcanii str. DS-2 ATCC 29605 (T)' : 0.03648 ) : 0.09112 , ('<env.SBAR16> Santa Barbara Channel bacterioplankton DNA clone SBAR16' : 0.19448 , '<Tpl.acidop> Thermoplasma acidophilum str. 122-1B2' : 0.22004 ) : 0.04224 ) : 0.10775 , '<Arg.fulgid> Archaeoglobus fulgidus str. VC-16 DSM 4304 (T)' : 0.04075 ) : 0.05544 , ('<Mb.formici> Methanobacterium formicicum DSM 1312' : 0.03067 , '<Mt.fervid1> Methanothermus fervidus' : 0.19624 ) : 0.01978 ) : 0.0947 , '<Tc.celer> Thermococcus celer str. VU 13 DSM 2476 (T)' : 0.00981 ) : 0.05532 , ('<Mc.vanniel> Methanococcus vannielii str. EY33' : 0.02484 , '<Mc.jannasc> Methanococcus jannaschii str. JAL-1 DSM 2661 (T)' : 0.1614 ) : 0.00857 ) : 0.02807 , '<Mpy.kand11> Methanopyrus kandleri str. av19 DSM 6324 (T)' : 0.09845 ) : 0.02703 , ('<env.pJP27> Mud Volcano area of Yellowstone NP ("Black Pool") hot spring DNA clone pJP27' : 0.06783 , ('<env.SBAR12> Santa Barbara Channel bacterioplankton DNA clone SBAR12' : 0.1046 , '<env.pJP89> Mud Volcano area of Yellowstone NP ("Black Pool") hot spring DNA clone pJP89' : 0.28523 ) : 0.01132 , ('<Tmf.penden> Thermofilum pendens str. Hvv3 DSM 2475 (T)' : 0.04404 , ('<Sul.acalda> Sulfolobus acidocaldarius str. 98-3 ATCC 33909 (T)' : 0.04024 , '<Thp.tenax> Thermoproteus tenax' : 0.15875 ) : 0.02106 ) : 0.09273 ) : 0.20883 ) : 0.03789 ) : 0.31178 , ('<Aqu.pyroph> Aquifex pyrophilus str. Kol5a' : 0.20649 , ('<Tl.maritim> Thermotoga maritima str. MSB8 DSM 3109 (T)' : 0.01001 , '<Fer.island> Fervidobacterium islandicum str. H-21 DSM 5733 (T)' : 0.16351 ) : 0.23062 , (('<Mei.ruber4> Meiothermus ruber str. Loginova 21 ATCC 35948 (T)' : 0.14908 , '<D.radiodur> Deinococcus radiodurans ATCC 35073' : 0.19907 ) : 0.08298 , ('<Cfx.aurant> Chloroflexus aurantiacus str. J-10-fl ATCC 29366 (T)' : 0.1976 , '<Tmc.roseum> Thermomicrobium roseum ATCC 27502 (T)' : 0.36297 ) : 0.11213 ) : 0.01165 , (((((((((((('<Acp.laidla> Achaeoplasma laidlawii str. JAI1' : 0.11002 , '<C.ramosum> Clostridium ramosum str. 113-I ATCC 25582 (T)' : 0.30774 ) : 0.00736 , '<M.capricol> Mycoplasma capricolum ATCC 27343 (T) [gene=rrnB]' : 0.38452 ) : 0.10528 , '<Stc.therm3> Streptococcus thermophilus DSM 20617 (T)' : 0.05073 ) : 0.15065 , '<Eco.faecal> Enterococcus faecalis' : 0.0306 ) : 0.01738 , ('<L.casei> Lactobacillus casei subsp. casei ATCC 393 (T)' : 0.13937 , '<L.delbruck> Lactobacillus delbrueckii subsp. delbrueckii str. Calvert ATCC 9649 (T)' : 0.04809 ) : 0.01852 ) : 0.02217 , '<Lis.monoc3> Listeria monocytogenes' : 0.02418 ) : 0.0404 , '<B.cereus4> Bacillus cereus IAM 12605 (T)' : 0.06989 ) : 0.0034 , ('<B.subtilis> Bacillus subtilis str. 168' : 0.05051 , '<B.stearoth> Bacillus stearothermophilus NCDO 1768 (T)' : 0.05959 ) : 0.0075 ) : 0.12658 , '<Eub.barker> Eubacterium barkeri ATCC 25849 (T)' : 0.28781 ) : 0.0097 , ('<C.quercico> Clostridium quercicolum ATCC 25974 (T)' : 0.13519 , '<Hel.chlor2> Heliobacterium chlorum ATCC 35205 (T)' : 0.1075 ) : 0.01024 ) : 0.01183 , ('<Fus.nuclea> Fusobacterium nucleatum subsp. nucleatum ATCC 25586 (T)' : 0.08593 , ('<Stm.ambofa> Streptomyces ambofaciens' : 0.06051 , ('<Cor.xerosi> Corynebacterium xerosis ATCC 373 (T)' : 0.10315 , ('<Bif.bifidu> Bifidobacterium bifidum ATCC 29521 (T)' : 0.29842 , '<Arb.globif> Arthrobacter globiformis str. 168 DSM 20124 (T)' : 0.12957 ) : 0.06797 ) : 0.00748 ) ;
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**Docket 010AUS; USSN 10/057,270; Figure 10A-10C** The representative prokaryotic phylogenetic tree in Newick format.

**Figure 10B**

0.3137 ) : 0.01738 ) : 0.00511 , ('<C.leptum> Clostridium leptum ATCC 29065 (T)' : 0.16126 , ('<C.butyric4> Clostridium butyricum str. E.VL3.6.1 NCIMB 8082' : 0.06037 , '<C.pasteuri> Clostridium pasteurianum ATCC 6013 (T)' : 0.07626 ) : 0.38023 ) : 0.02432 ) : 0.01262 , (((((((('<Rub.gelat2> Rubrivivax gelatinosus str. ATH 2.2.1 ATCC 17011 (T)' : 0.07169 , '<Spr.voluta> Spirillum volutans ATCC 19554 (T)' : 0.06661 ) : 0.00462 , '<Rcy.purpur> Rhodocyclus purpureus str. 6770 DSM 168 (T)' : 0.04015 ) : 0.02165 , '<Nis.gonor1> Neisseria gonorrhoeae str. B 5025 NCTC 8375 (T)' : 0.19789 ) : 0.01431 , '<Ste.maltop> Stenotrophomonas maltophilia ATCC 13637 (T)' : 0.24098 ) : 0.02299 , ('<E.coli> Escherichia coli [gene=rrnB operon]' : 0.05825 , '<Ps.aerugi3> Pseudomonas aeruginosa DSM 50071 (T)' : 0.63646 ) : 0.03524 ) : 0.04488 , '<Alm.vinosm> Allochromatium vinosum ATCC 17899 (T)' : 0.0233 ) : 0.04869 , '<Hrh.halch2> Halorhodospira halochloris str. A ATCC 35916 (T)' : 0.05948 ) : 0.08019 , (('<R.rubrum3> Rhodospirillum rubrum str. ATH 1.1.1; S.1 ATCC 11170 (T)' : 0.04904 , '<Azs.brsi2> Azospirillum brasilense str. Sp 7 NCIMB 11860 (T)' : 0.3086 ) : 0.01343 , ('<Ric.prowaz> Rickettsia prowazekii str. Breinl ATCC VR-142 (T) (alpha purple bacterium)' : 0.1406 , '<Spg.capsul> Sphingomonas capsulata ATCC 14666 (T)' : 0.13872 ) : 0.02068 , ('<Rlib.legum8> Rhizobium leguminosarum IAM 12609 (T)' : 0.01576 , ('<Bdr.japoni> Bradyrhizobium japonicum LMG 6138 (T)' : 0.05736 , '<Rm.vanniel> Rhodomicrobium vannielii str. EY33 ATCC 51194' : 0.093 ) : 0.04263 ) : 0.00617 ) : 0.03466 ) : 0.06772 ) : 0.00546 , (('<Myx.xantha> Myxococcus xanthus str. DK1622' : 0.11263 , '<Dsb.postga> Desulfobacter postgatei str. 2 ac 9 DSM 2034 (T)' : 0.19098 ) : 0.01154 , ('<Dsv.desulf> Desulfovibrio desulfuricans subsp. desulfuricans ATCC 27774' : 0.01563 , ('<Bde.stolpi> Bdellovibrio stolpii str. UK12 ATCC 27052 (T)' : 0.05967 , ('<Cam.jejun5> Campylobacter jejuni subsp. jejuni str. TGH 9011 ATCC 43431' : 0.01753 , ('<Wln.succi2> Wolinella succinogenes str. 602W (FDC) ATCC 29543 (T)' : 0.05551 , '<Hlb.pylor6> Helicobacter pylori ATCC 43504 (T)' : 0.02351 ) : 0.18884 ) : 1.11671 ) : 0.18947 ) : 0.01602 ) : 0.15633 ) : 0.01513 , (((((((('<Trp.pallid> Treponema pallidum str. Nichols' : 0.14543 , '<Spi.stenos> Spirochaeta stenostrepta str. Z1 ATCC 25083 (T)' : 0.03623 ) : 0.03698 , '<Bor.burgdo> Borrelia burgdorferi str. B31 ATCC 35210 (T)' : 0.3604 ) : 0.0859 , '<Spi.haloph> Spirochaeta halophila str. RS1 ATCC 29478 (T)' : 0.02473 ) : 0.01206 , '<Brs.hyodys> Brachyspira hyodysenteriae str. B204 ATCC 31212' : 0.43546 ) : 0.04129 , ('<Lpn.illini> Leptonema illini str. 3055' : 0.07041 , '<Lps.interK> Leptospira interrogans str. Kennewicki, serovar pomona' : 0.16902 ) : 0.05013 ) : 0.01817 , ('<Fib.suc585> Fibrobacter succinogenes subsp. succinogenes str. S85 ATCC 19169 (T)' : 0.23142 , '<Acbt.capsl> Acidobacterium capsulatum str. 161' : 0.21099 ) : 0.03073 ) : 0.0094 , (((((((('<Syn.6301> Synechococcus sp. PCC 6301' : 0.12285 , '<Nost.muscr> Nostoc muscorum PCC 7120' : 0.06977 ) : 0.01225 , ('<Zea\_mays\_C> Zea mays (maize; corn; Indian corn) -- chloroplast' : 0.145 , '<Olst.lut\_C> Olisthodiscus luteus (stramenopile) -- chloroplast' : 0.3525 ) : 0.09491 ) : 0.012 , '<Glb.violac> Gloeobacter violaceus PCC 7421' : 0.07279 ) : 0.01171 , ('<env.MC18> Mount Coot-tha region (Brisbane, Australia) 5-10cm depth soil DNA clone MC 18' : 0.01409 , ('<Chd.psitta> Chlamydophila psittaci str. 6BC ATCC VR-125 (T)' : 0.36004 , '<Pir.staley> Pirellula staleyi ATCC 27377' : 0.34247 ) : 0.25993 ) : 0.1121 ) : 0.03258 , ('<Chl.linico> Chlorobium limicola str. 8327' : 0.1389 , ('<Tnm.lapsum> Thermonema lapsum ATCC Docket 010AUS; USSN 10/057,270; Figure 10A-10C The representative prokaryotic phylogenetic tree in Newick format.

43542 (T)' : 0.0332 , ('<Flx.litora> Flexibacter litoralis str. Lewin SIO-4 ATCC 23117 (T)' : 0.01576 , ('<Cy.hutchin> Cytophaga hutchinsonii str. D465 (P.H.A. Sneath) ATCC 33406 (T)' : 0.0073 , ('<Prb.diffllu>

**Figure 10C**

Persicobacter diffluens str. Lewin LIM-1 ATCC 23140' : 0.00585 , ('<Sap.grandi> Saprospira grandis ATCC 23119 (T)' : 0.02768 , ('<Flx.canada> Flexibacter canadensis ATCC 29591 (T)' : 0.03254 , (('<Bac.fragil> Bacteroides fragilis ATCC 25285 (T)' : 0.04826 , ('<Prv.rumcol> Prevotella ruminicola subsp. ruminicola ATCC 19189 (T)' : 0.20539 ) : 0.02821 , ('<Cy.lytica> Cytophaga lytica str. LIM-21 ATCC 23178 (T)' : 0.14365 , '<Emb.brevi2> Empedobacter brevis ATCC 14234' : 0.0913 ) : 0.35994 ) : 0.12199 ) : 0.33291 ) : 0.47588 ) : 0.14622 ) : 0.18424 ) : 0.08878 ) : 0.30465 ) : 0.05104 ) : 0.00825 ) : 0.02261 ) : 0.00329 ) : 0.56238 ) : 0.52312 ) : 0.05444 ) : 0.31178 ); **Docket 010AUS; USSN 10/057,270; Figure 10A-10C** The representative prokaryotic phylogenetic tree in Newick format.